

AMENDMENTS TO THE CLAIMS

1. (Canceled)
2. (Canceled)
3. (Canceled)
4. (Canceled)
5. (Canceled)
6. (Canceled)
7. (Canceled)
8. (Canceled)
9. (Canceled)
10. (Canceled)
11. (Canceled)
12. (Currently Amended) A method for inferring genomic sequences unique to at least one set of organisms other than a set of organisms under investigation, the method comprising:
 - obtaining genomic data characteristic of a set of organisms under investigation;
 - formatting the genomic data into at least one query-length sequence, each query-length sequence being of a format compatible with a similarity search engine;
 - searching a selected genomic database using the query-length sequence and the similarity search engine;

the selected genomic database containing genomic data from a plurality of organisms;

parsing the results of the search for those sequences having homology above a threshold with at least one set of organisms other than the set under investigation,

outputting to memory an identity of those sequences having homology above a threshold with at least one set of organisms other than the set under investigation.

13. (Currently amended) A computer program for inferring genomic sequences unique to a at least one set of organisms other than a set of organisms under investigation, the computer program product comprising:

a computer-readable medium;

a genomic data interface module, stored on the medium and operable to couple to a source of genomic data to receive genomic data characteristic of a set of organisms under investigation;

a formatting module, stored on the medium and operable to format received genomic data into at least one query-length sequence, each query-length sequence being of a format compatible with a similarity search engine;

a search interface module, stored on the medium and operable to interface with the similarity search engine to submit the query-length sequence to a selected genomic database containing genomic data from a substantial plurality of organisms ~~the search engine~~; and

a search results parsing module, stored on the medium and operable to parse the results of the search for those sequences having homology above a threshold with at least one set of organisms other than the set under investigation, and to output to memory an identity of those sequences having homology above a threshold with at least one set of organisms other than the set under investigation.